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**WAPLE**  
 \*\*\*\*\* (TM)  
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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run On: Thu Oct 31 08:33:41 1996; MasPar time 295.79 Seconds

Tabular output not generated. 1189.730 Million cell updates/sec

Title: >PCT-US96-14730-5

Description: (1-463) from PCTUS9614730.seq

Perfect Score: 463

N.A. Sequence: 1 CAATACGATATTACCGAATA.....CCGGTGAAGTACGAGSTC 463  
 Comp: GTTATGCTATAATGGCTTAT.....GGCCACTTCATTCGTCWAG

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 270440 seqs, 38002776 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: embi-new3

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN

9:PRI1 10:PRI2 11:PRO 12:ROD 13:SYN 14:UNC 15:VRT

16:VRL1 17:VIR2

genbank92

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7

25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5

32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG

39:PLN1 40:PLN2 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PLN7

46:PLN8 47:PRI1 48:PRI2 49:PRI3 50:PRI4 51:PRI5 52:PRI6

53:PRI7 54:PRI8 55:PRI9 56:PRI10 57:PRI11 58:PRI12

59:PRI13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6

66:ROD7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3

73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

genbank-new1

80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PLN 86:PRI

87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT

u-emb145\_92

93:parti

Statistics: Mean 11.110; Variance 8.217; scale 1.352

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description	Pred. No.
1	294	63.5	2884	45	TOMHMG2A	Tomato 3-hydroxy-3-me 3.83e-142
c 2	36	7.8	1095	40	DDICSA	Dictyostellum discoid 2.69e-03
c 3	36	7.8	3700	28	DGPG80G	D. discoideum gp80 gen 2.69e-03

4	33	7.1	14001	5	PFCOMPIRB	P. falciparum complete	4.75e-02
5	33	7.1	14001	82	PFCOMPIRB	P. falciparum complete	4.75e-02
6	32	6.9	1283	28	DDDD31GE	D. discoideum (AX-4) D	1.21e-01
7	32	6.9	2379	5	DD31	D. discoideum culminat	1.21e-01
8	31	6.7	6615	41	MISDCYTB	S. douglasii gene for	3.03e-01
9	30	6.5	854	46	YSLMTIG08	Yeast (T. glabrata) mi	7.52e-01
10	30	6.5	854	41	MITGIRN6	Torulopsis glabrata	7.52e-01
c 11	30	6.5	865	31	PLU39369	Parastenopalmata 16	7.52e-01
c 12	30	6.5	1868	76	VSVGLXPQ	Vesicular stomatitis	7.52e-01
13	29	6.3	116	35	A08900	H. sapiens (haplotype	1.84e+00
14	29	6.3	3000	40	DDIGP24	D. discoideum glycopro	1.84e+00
15	29	6.3	3075	32	XPFNAPOL	P. falciparum gene for	1.84e+00
16	29	6.3	7038	31	PFGP195A	Plasmodium falciparum	1.84e+00
17	29	6.3	8633	31	PFPMDR1	P. falciparum pfmdrl g	1.84e+00
18	29	6.3	15421	5	PFCOMPIRA	P. falciparum complete	1.84e+00
19	29	6.3	15421	82	PFCOMPIRA	Plasmodium falciparum	1.84e+00
20	29	6.3	2243	31	PFAVAR23A	Vesicular stomatitis	1.84e+00
21	28	6.0	1860	76	VSVGLYPR	D. discoideum emma pro	4.42e+00
22	28	6.0	1950	28	DDBCMA	Saccharomyces cerevis	4.42e+00
23	28	6.0	2858	46	YSCMTG18	D. malanogaster positi	4.42e+00
24	28	6.0	5726	29	DROANTPS2	P. falciparum complete	4.42e+00
25	28	6.0	14001	82	PFCOMPIRB	P. falciparum complete	4.42e+00
26	28	6.0	14001	5	PFCOMPIRB	D. virginiana mitochon	4.42e+00
27	28	6.0	17084	33	DVMTGNME	Human DNA sequence fr	4.42e+00
28	28	6.0	28951	86	HSL161C2	Human DNA sequence fr	4.42e+00
29	28	6.0	28951	10	HSL161C2	Caenorhabditis elegans	4.42e+00
30	28	6.0	34037	28	CELF43C9	S. cerevisiae mitochon	4.42e+00
31	28	6.0	34860	28	CELR173	Drosophila satellite	1.05e-01
32	28	6.0	78520	93	MISCCG	Toxotrypana curvicaud	1.05e-01
33	27	5.8	525	29	DSMAT02	B. juncea DNA for 2S s	1.05e-01
34	27	5.8	872	32	TCU39381	Dictyostellum discoid	1.05e-01
35	27	5.8	1137	39	B12SSTP	Yeast mitochondrial D	1.05e-01
36	27	5.8	1305	40	DDICALA	Vesicular stomatitis	1.05e-01
37	27	5.8	1722	41	MISC38	Brassica napus nap8 g	1.05e-01
38	27	5.8	1861	76	VSVGLYPO	C. caldarium operon of	1.05e-01
39	27	5.8	1993	39	BNNAPIN	Mus musculus small he	1.05e-01
40	27	5.8	2160	40	CCRUBISCO	Nicotiana glutinosa v	1.05e-01
41	27	5.8	3058	62	MUSHSP25A	Plasmodium falciparum	1.05e-01
42	27	5.8	3289	39	BNNAPPA	Trypanosoma brucei br	1.05e-01
43	27	5.8	7158	42	NGU15605		
44	27	5.8	10213	31	PFU27338		
45	27	5.8	23016	32	TRBKPGEN		

#### ALIGNMENTS

RESULT	1	TOMHMG2A	2884 bp	DNA	PLN	14-OCT-1992
LOCUS		Tomato 3-hydroxy-3-methyl glutaryl coenzyme A reductase (hmg2)				
DEFINITION		gene, complete cds.				
ACCESSION		M63642				
NID		g170451				
KEYWORDS		3-hydroxy-3-methylglutaryl coenzyme A reductase.				
SOURCE		Lycopersicon esculentum (strain VFNT cherry) DNA.				
ORGANISM		Lycopersicon esculentum				
REFERENCE		Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida; Asteridae; Solanales; Solanaceae.				
AUTHORS		1 (sites)				
TITLE		Yang, Z., Park, H. S., Lacy, G. H. and Cramer, C. L.				
JOURNAL		Differential activation of potato 3-hydroxy-3-methyl glutaryl				
MEDLINE		coenzyme A reductase genes by wounding and pathogen challenge				
REFERENCE		Plant Cell 3, 397-409 (1991)				
AUTHORS		2 (sites)				
TITLE		Park, H. S., Denbow, C. J. and Cramer, C. L.				
JOURNAL		Structure and nucleotide sequence of tomato HMG2 encoding				
MEDLINE		3-hydroxy-3-methyl-glutaryl coenzyme A reductase				
REFERENCE		Plant Mol. Biol. 20, 327-331 (1992)				
FEATURES		93004487				
NCBI gi:		170451				
Location/Qualifiers		1..2884				
source		/organism="Lycopersicon esculentum"				

Query Match	63.5%	Score	294;	DB	45;	Length	2884;
Best Local Similarity	99.4%	Pred.	NO.	3.83e-142;			
Matches	306;	Conservative	0;	Mismatches	0;	Indels	2;
Gaps	1;						

  

Db	1	taatagcccgagtctgatacccgaattttcacacttgacgcagtcgaactgtgactataaaa	60
Qy	147	TAA TAGGCCCGAGTTCGTATCCAAAATATTTTACACTTTGACCAGTCACTTGCACTATATAAA	206
Db	61	cttctactcacaagaattaaaaaaagaaagatatatttgtaaaaagataaactccat	120
Qy	207	CITTTACTCAAAAAATTA AAAA AAGAAAGATATATTGTGTAAGAAGATAATACTCCAT	266
Db	121	tcaaaataaaaaatgaaaaaacgtcgcgcgcgcgcgggtctctctataaaatcatttc	180
Qy	267	TCAAATATAAAATGAAAAAAGTCACGCGCAGCACCGGGTTCT--ATAAATACATTTCT	324
Db	181	ctacatctctctctctcscatcccccatcactctctttttaacaattatacttgtcaat	240
Qy	325	CTACATCTTCTCTCTCTCACTCCCACATCTCTCTTTTAACAATATATAGTTGTCAAT	384
Db	241	caccaatccacaaacacactttttctctctcttttctcaccgcgcgcgcagacttac	300
Qy	385	CATCATCCCCAACAAACACATTTTTTCTCTCTCTTTTTCTCTCACCGCGGCAGACTTAC	444
Db	301	cgggtgaa	308
Qy	445	CGGTGAAA	452

  

RESULT	2
LOCUS	DITCSA 1095 bp DNA PLN 16-JUL-1992
DEFINITION	Dictyostellium discoideum CAMP-regulated promoter (csa) gene,

[illegible]